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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/537,710B

DATE: 07/31/2002

TIME: 10:02:37

Input Set : A:\EP.txt

Output Set: N:\CRF3\07312002\I537710B.raw

```

3 <110> APPLICANT: Dahlqvist, Andres
4      Stahl, Ulf
5      Lenman, Marit
6      Banas, Antoni
7      Ronne, Hans
9 <120> TITLE OF INVENTION: A new class of enzymes in the biosynthetic pathway for the
production
10      of
11      triacylglycerol and recombinant DNA molecules encoding these enzymes
13 <130> FILE REFERENCE: BASFnae337799PCT1-15
15 <140> CURRENT APPLICATION NUMBER: US 09/537,710B
17 <141> CURRENT FILING DATE: 2000-03-30
19 <150> PRIOR APPLICATION NUMBER: EP 99106656.4
20 <151> PRIOR FILING DATE: 1999-04-01
22 <160> NUMBER OF SEQ ID NOS: 31
24 <170> SOFTWARE: WordPerfect version 6.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1986
28 <212> TYPE: DNA
29 <213> ORGANISM: Saccharomyces cerevisiae
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(1983)
35 <400> SEQUENCE: 1
37 atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48
38 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
39 1 5 10 15
41 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
42 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
43 20 25 30
45 aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
46 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
47 35 40 45
49 att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
50 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
51 50 55 60
53 aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240
54 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
55 65 70 75 80
57 att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt 288
58 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
59 85 90 95
61 ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt 336
62 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe

```

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Input Set : A:\EP.txt  
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63	100	105	110	
65 gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt	384			
66 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val				
67 115 120 125				
69 ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac	432			
70 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn				
71 130 135 140				
73 tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt	480			
74 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly				
75 145 150 155 160				
77 aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta	528			
78 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val				
79 165 170 175				
81 atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att	576			
82 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile				
83 180 185 190				
85 gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg	624			
86 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp				
87 195 200 205				
89 gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg	672			
90 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp				
91 210 215 220				
93 ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac	720			
94 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn				
95 225 230 235 240				
97 ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc	768			
98 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile				
99 245 250 255				
101 gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att	816			
102 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile				
103 260 265 270				
105 ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt	864			
106 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu				
107 275 280 285				
109 gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag	912			
110 Ala Tyr Leu Asp Leu Glu Arg Asp Arg Tyr Phe Thr Lys Leu Lys				
111 290 295 300				
113 gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta	960			
114 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu				
115 305 310 315 320				
117 att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg	1008			
118 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp				
119 325 330 335				
121 gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt	1056			
122 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val				
123 340 345 350				
125 aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc	1104			
126 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly				
127 355 360 365				

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129	gct	cca	aag	gca	gtt	cca	gct	cta	att	agt	ggt	gaa	atg	aaa	gat	acc	1152
130	Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr	
131		370					375					380					
133	att	caa	tta	aat	acg	tta	gcc	atg	tat	ggt	ttg	gaa	aag	ttc	ttc	tca	1200
134	Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser	
135	385				390					395						400	
137	aga	att	gag	aga	gta	aaa	atg	tta	caa	acg	tgg	ggt	ggt	ata	cca	tca	1248
138	Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser	
139				405						410					415		
141	atg	cta	cca	aag	gga	gaa	gag	gtc	att	tgg	ggg	gat	atg	aag	tca	tct	1296
142	Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser	
143				420						425					430		
145	tca	gag	gat	gca	ttg	aat	aac	aac	act	gac	aca	tac	ggc	aat	ttc	att	1344
146	Ser	Glu	Asp	Ala	Leu	Asn	Asn	Asn	Thr	Asp	Thr	Tyr	Gly	Asn	Phe	Ile	
147			435				440						445				
149	cga	ttt	gaa	agg	aat	acg	agc	gat	gct	ttc	aac	aaa	aat	ttg	aca	atg	1392
150	Arg	Phe	Glu	Arg	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Lys	Asn	Leu	Thr	Met	
151		450				455					460						
153	aaa	gac	gcc	att	aac	atg	aca	tta	tcg	ata	tca	cct	gaa	tgg	ctc	caa	1440
154	Lys	Asp	Ala	Ile	Asn	Met	Thr	Leu	Ser	Ile	Ser	Pro	Glu	Trp	Leu	Gln	
155	465				470					475					480		
157	aga	aga	gta	cat	gag	cag	tac	tcg	ttc	ggc	tat	tcc	aag	aat	gaa	gaa	1488
158	Arg	Arg	Val	His	Glu	Gln	Tyr	Ser	Phe	Gly	Tyr	Ser	Lys	Asn	Glu	Glu	
159				485					490						495		
161	gag	tta	aga	aaa	aat	gag	cta	cac	cac	aag	cac	tgg	tcg	aat	cca	atg	1536
162	Glu	Leu	Arg	Lys	Asn	Glu	Leu	His	His	Lys	His	Trp	Ser	Asn	Pro	Met	
163				500					505						510		
165	gaa	gta	cca	ctt	cca	gaa	gct	ccc	cac	atg	aaa	atc	tat	tgt	ata	tac	1584
166	Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr	
167			515				520						525				
169	ggg	gtg	aac	aac	cca	act	gaa	agg	gca	tat	gta	tat	aag	gaa	gag	gat	1632
170	Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp	
171		530				535					540						
173	gac	tcc	tct	gct	ctg	aat	ttg	acc	atc	gac	tac	gaa	agc	aag	caa	cct	1680
174	Asp	Ser	Ser	Ala	Leu	Asn	Leu	Thr	Ile	Asp	Tyr	Glu	Ser	Lys	Gln	Pro	
175	545				550					555					560		
177	gta	ttc	ctc	acc	gag	ggg	gac	gga	acc	gtt	ccg	ctc	gtg	gcg	cat	tca	1728
178	Val	Phe	Leu	Thr	Glu	Gly	Asp	Gly	Thr	Val	Pro	Leu	Val	Ala	His	Ser	
179				565					570						575		
181	atg	tgt	cac	aaa	tgg	gcc	cag	ggt	gct	tca	ccg	tac	aac	cct	gcc	gga	1776
182	Met	Cys	His	Lys	Trp	Ala	Gln	Gly	Ala	Ser	Pro	Tyr	Asn	Pro	Ala	Gly	
183				580				585							590		
185	att	aac	gtt	act	att	gtg	gaa	atg	aaa	cac	cag	cca	gat	cga	ttt	gat	1824
186	Ile	Asn	Val	Thr	Ile	Val	Glu	Met	Lys	His	Gln	Pro	Asp	Arg	Phe	Asp	
187			595				600						605				
189	ata	cgt	ggt	gga	gca	aaa	agc	gcc	gaa	cac	gta	gac	atc	ctc	ggc	agc	1872
190	Ile	Arg	Gly	Gly	Ala	Lys	Ser	Ala	Glu	His	Val	Asp	Ile	Leu	Gly	Ser	
191		610				615						620					
193	gcg	gag	ttg	aac	gat	tac	atc	ttg	aaa	att	gca	agc	ggt	aat	ggc	gat	1920

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194 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
195 625 630 635 640
197 ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
198 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
199 645 650 655
201 atg ccc ttc cca atg taa 1986
202 Met Pro Phe Pro Met
203 660
206 <210> SEQ ID NO: 2
207 <211> LENGTH: 661
208 <212> TYPE: PRT
209 <213> ORGANISM: Saccharomyces cerevisiae
211 <400> SEQUENCE: 2
212 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
213 1 5 10 15
215 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
216 20 25 30
218 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
219 35 40 45
221 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
222 50 55 60
224 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
225 65 70 75 80
227 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
228 85 90 95
230 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
231 100 105 110
233 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
234 115 120 125
236 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
237 130 135 140
239 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
240 145 150 155 160
242 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
243 165 170 175
245 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
246 180 185 190
248 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
249 195 200 205
251 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
252 210 215 220
254 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
255 225 230 235 240
257 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
258 245 250 255
260 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
261 260 265 270
263 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
264 275 280 285

```

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```

266 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
267      290                      295                      300
269 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
270 305                      310                      315                      320
272 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
273                      325                      330                      335
275 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
276                      340                      345                      350
278 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
279                      355                      360                      365
281 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
282      370                      375                      380
284 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
285 385                      390                      395                      400
287 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
288                      405                      410                      415
290 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
291                      420                      425                      430
293 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
294                      435                      440                      445
296 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
297      450                      455                      460
299 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
300 465                      470                      475                      480
302 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
303                      485                      490                      495
305 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
306                      500                      505                      510
308 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
309                      515                      520                      525
311 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
312      530                      535                      540
314 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
315 545                      550                      555                      560
317 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
318                      565                      570                      575
320 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
321                      580                      585                      590
323 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
324                      595                      600                      605
326 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
327      610                      615                      620
329 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
330 625                      630                      635                      640
332 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
333                      645                      650                      655
335 Met Pro Phe Pro Met
336      660
340 <210> SEQ ID NO: 3

```

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Input Set : A:\EP.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 2363  
Seq#:7; N Pos. 601,627  
Seq#:7; Xaa Pos. 116,121  
Seq#:9; N Pos. 15,45,83,103,107,112,210  
Seq#:25; N Pos. 240,385  
Seq#:25; Xaa Pos. 41,89  
Seq#:26; N Pos. 601,627  
Seq#:26; Xaa Pos. 116,121  
Seq#:28; N Pos. 15,45,83,103,107,112,210

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9

## VERIFICATION SUMMARY

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Input Set : A:\EP.txt

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L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2340  
L:658 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:662 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:384  
L:703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:552  
L:705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:612  
L:753 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
L:754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:60  
L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:180  
L:2277 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25  
L:2291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:215  
L:2292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:263  
L:2303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:359  
L:2304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:402  
L:2327 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
L:2357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:384  
L:2368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:552  
L:2370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:612  
L:2409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0  
L:2410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:60  
L:2412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:180